

0360 0200  
**RAW SEQUENCE LISTING**  
**PATENT APPLICATION US/08/896,589****TEAM 8**  
DATE: 09/03/97  
TIME: 13:27:20

INPUT SET: S20087.raw

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

  
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## SEQUENCE LISTING

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3 (1) General Information  
45 (i) APPLICANT: Burnham, Martin K.  
67 (ii) TITLE OF THE INVENTION: NOVEL XANTHINE PHOSPHORIBOSYL  
8 TRANSFERASE  
910 (iii) NUMBER OF SEQUENCES: 6  
11

## 12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Dechert Price &amp; Rhoads

14 (B) STREET: 997 Lenox Drive, Building 3, Suite 210

15 (C) CITY: Lawrenceville

16 (D) STATE: NJ

17 (E) COUNTRY: USA

18 (F) ZIP: 08543  
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## 20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette

22 (B) COMPUTER: IBM Compatible

23 (C) OPERATING SYSTEM: DOS

24 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
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## 26 (vi) CURRENT APPLICATION DATA:

27 (A) APPLICATION NUMBER:

28 (B) FILING DATE:

29 (C) CLASSIFICATION:  
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## 31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER:

33 (B) FILING DATE:  
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## 37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Bloom, Allen

39 (B) REGISTRATION NUMBER: 29,135

40 (C) REFERENCE/DOCKET NUMBER:  
41

## 42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 609-520-3214

44 (B) TELEFAX: 609-520-3259

45 (C) TELEX:  
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# RAW SEQUENCE LISTING

## PATENT APPLICATION US/08/896,589

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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAATTAT	TAGAAGAGCG	CATCCTCAAG	GATGGGCATA	TCTTGGGTGA	TAACATCCTC	60
AAGGTAGATT	CCTTTTAAAC	CCACCAAGTT	GACTTTAGCT	TGATGCGAGA	GATTGGTAAG	120
GTTTTTGCGG	AAAAATTTGC	TGCTACTGGC	ATTACCAAGG	TCGTAACCAT	TGAAGCGTCG	180
GGTATTGCC	CAGCCGTTTT	TACAGCTGAA	GCCTTAAACG	TTCCCATGAT	TTTCGCCAAA	240
AAAGCTAAGA	ACATCACCAT	GAACGAAGGC	ATCTTAACTG	CTCAAGTCTA	CTCCTTTACC	300
AAGCAGGTGA	CCAGCACTGT	TTCTATCGCT	GGAAAATTCC	TCTCACCAGA	GGACAAGGTT	360
TTGATTATCG	ACGATTTCCT	TGCTAATGGC	CAAGCTGCTA	AAGGCTTGAT	TCAAATCATC	420
GAACAGGCCG	GTGCCACAGT	CCAAGCTATC	GGTATCGTGA	TTGAGAAAATC	CTTCCAAGAT	480
GGTCGTGATT	TGCTTGAAAA	AGCAGGCTAC	CCTGTCCTAT	CACTTGCTCG	CTTGGATCGT	540
TTTGAAAATG	GTCAGGTCGT	ATTTAAGGAG	GCAGATCTCT	AA		582

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Leu	Leu	Glu	Glu	Arg	Ile	Leu	Lys	Asp	Gly	His	Ile	Leu	Gly
1				5					10					15	
Asp	Asn	Ile	Leu	Lys	Val	Asp	Ser	Phe	Leu	Thr	His	Gln	Val	Asp	Phe
			20					25					30		
Ser	Leu	Met	Arg	Glu	Ile	Gly	Lys	Val	Phe	Ala	Glu	Lys	Phe	Ala	Ala
		35					40					45			
Thr	Gly	Ile	Thr	Lys	Val	Val	Thr	Ile	Glu	Ala	Ser	Gly	Ile	Ala	Pro
	50					55					60				
Ala	Val	Phe	Thr	Ala	Glu	Ala	Leu	Asn	Val	Pro	Met	Ile	Phe	Ala	Lys
	65				70					75				80	
Lys	Ala	Lys	Asn	Ile	Thr	Met	Asn	Glu	Gly	Ile	Leu	Thr	Ala	Gln	Val
			85						90					95	
Tyr	Ser	Phe	Thr	Lys	Gln	Val	Thr	Ser	Thr	Val	Ser	Ile	Ala	Gly	Lys
		100						105					110		
Phe	Leu	Ser	Pro	Glu	Asp	Lys	Val	Leu	Ile	Ile	Asp	Asp	Phe	Leu	Ala
		115					120				125				
Asn	Gly	Gln	Ala	Ala	Lys	Gly	Leu	Ile	Gln	Ile	Ile	Glu	Gln	Ala	Gly
	130					135					140				
Ala	Thr	Val	Gln	Ala	Ile	Gly	Ile	Val	Ile	Glu	Lys	Ser	Phe	Gln	Asp

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100      145      150      155      160
101 Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala
102      165      170      175
103 Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp
104      180      185      190
105 Leu
106
107

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

119 ATGAAATTAT TAGAAGAGCG CATCCTCAAG GATGGGCATA TCTTGGGTGA TAACATCCTC      60
120 AAGGTAGATT CCTTTTAAAC CCACCAAGTT GACTTTAGCT TGATGCGAGA GATTGGTAAG      120
121 GTTTTTCGCG AAAAATTTGC TGCTACTGGC ATTACCAAGG TCGTAACCAT TGAAGCGTCG      180
122 GGTATTGCCC CAGCCGTTTT TACAGCTGAA GCCTTAAACG TTCCCATGAT TTTCGCCAAA      240
123 AAAGCTAAGA ACATCACCAT GAACGAAGGC ATCTTAACTG CTCAAGTCTA CTCCTTTACC      300
124 AAGCAGGTGA CCAGCACTGT TTCTATCGCT GGAAAAATTCC TCTCACCAGA GGACAAGGTT      360
125 TTGATTATCG ACGATTTCTT TGCTAATGGC CAAGCTGCTA AAGGCTTGAT TCAAATCATC      420
126 GAACAGGCCG GTGCCACAGT CCAAGCTATC GGTATCGTGA TTGAGAAATC CTTCCAAGAT      480
127 GGTGCGTATT TGCTTGAAAA AGCAGGCTAC CCTGTCCTAT CACTTGCTCG CTTGGATCGT      540
128 TTTGAAAATG GTCAGGTCGT ATTTAAGGAG GCAGATCTC      579
129

```

## (2) INFORMATION FOR SEQ ID NO:4:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

141 Met Lys Leu Leu Glu Glu Arg Ile Leu Lys Asp Gly His Ile Leu Gly
142 1      5      10      15
143 Asp Asn Ile Leu Lys Val Asp Ser Phe Leu Thr His Gln Val Asp Phe
144      20      25      30
145 Ser Leu Met Arg Glu Ile Gly Lys Val Phe Ala Glu Lys Phe Ala Ala
146      35      40      45
147 Thr Gly Ile Thr Lys Val Val Thr Ile Glu Ala Ser Gly Ile Ala Pro
148      50      55      60
149 Ala Val Phe Thr Ala Glu Ala Leu Asn Val Pro Met Ile Phe Ala Lys
150      65      70      75      80
151 Lys Ala Lys Asn Ile Thr Met Asn Glu Gly Ile Leu Thr Ala Gln Val
152      85      90      95

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/896,589

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153 Tyr Ser Phe Thr Lys Gln Val Thr Ser Thr Val Ser Ile Ala Gly Lys  
154 100 105 110  
155 Phe Leu Ser Pro Glu Asp Lys Val Leu Ile Ile Asp Asp Phe Leu Ala  
156 115 120 125  
157 Asn Gly Gln Ala Ala Lys Gly Leu Ile Gln Ile Ile Glu Gln Ala Gly  
158 130 135 140  
159 Ala Thr Val Gln Ala Ile Gly Ile Val Ile Glu Lys Ser Phe Gln Asp  
160 145 150 155 160  
161 Gly Arg Asp Leu Leu Glu Lys Ala Gly Tyr Pro Val Leu Ser Leu Ala  
162 165 170 175  
163 Arg Leu Asp Arg Phe Glu Asn Gly Gln Val Val Phe Lys Glu Ala Asp  
164 180 185 190  
165 Leu  
166  
167

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCTCAAGGT AGATTCCTTT TTAAC

25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTCCTTAAAT ACGACCTGAC

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/896,589**

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Line

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Original Text